

AMENDMENTS TO THE SPECIFICATION:

Please replace lines 25-32 on page 10, through lines 1-6 on page 11 with the following: with the following:

Fig.1 shows an example of the BAAV genome. (A) The genomes of BAAV(SEQ ID NO:1), AAV2 (SEQ ID NO:25),, AAV4 (SEQ ID NO:26), and AAV5 (SEQ ID NO:27), were aligned using MaeVeeter MACVECTOR™ (Oxford Molecular). Nucleotides identical in at least 2 AAV serotypes are displayed boxed and shaded. (B) Phylogenetic relationship of BAAV to other serotypes is illustrated by an unrooted tree diagram.

Fig.2 shows an example of a BAAV ITR(SEQ ID NO:28). The sequence of the ITR is shown in hairpin configuration. The putative Rep binding site (SEQ ID NO:24) and TRS element (SEQ ID NO:14) are boxed. Sequence changes relative to the AAV5 ITR are annotated either above or below the BAAV sequence in bold letters.

Fig. 3 illustrated comparisons of Rep and V_{p1} VP1 amino acid sequences. The (A) rep Alignment of the amino acid sequences of BAAV Rep protein, AAV2 Rep protein (SEQ ID NO:29) and AAV5 Rep protein (SEQ ID NO:30) using MACVECTOR™. and (B) eap Alignment of the amino acid sequences of BAAV VP1 protein, AAV2 VP1 protein (SEQ ID NO:31) and AAV4 VP1 protein using MACVECTOR™. Cap protein ORFs of BAAV were aligned to the corresponding amino acid sequences of AAV2, AAV5 and AAV2, AAV respectively using MaeVeeter. Identical amino acids are indicated by a dark, shaded box, similar amino acids by a light, shaded box. Dashes indicate gaps in the sequence added by the alignment program. Phylogenetic relationship of (C) BAAV Rep and (D) V_{p1} VP1 to other AAV serotypes is illustrated by an unrooted tree diagram.